

SEQUENCE LISTINGS

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2623 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Rattus norvegicus

(B) TISSUE TYPE: Dorsal root ganglion

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 292..1909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

spasic Length: 2622

1 AGTGACAGCT GTGCGGGTGC TGATAAGGGA AGCCACAAGG AGACGATCGA

51 GGAGAGAGAC AAGCGGCAGC AGAGGCAGCA GCGACAGATG CAGCGCCGGG

101 GCTGCGGAGC TGCTGGGAGT GGGAGTGACG CCCCCACCTC GGGCCCCCAC

151 CCTGTCCCCA TCCTCCTCCT GGTGCCCCTG AGTTTAGAAG AGCAGCCGCT

201 GCCACCACCA CCACTCCGGA GGGCACCAGG GCTGCTGTCC AGGGAAGGAC

251 AGTAGCAGTG AGGCTCTGGC CAGTCCCAGC AGCCGGGGAC AGATGCCGAT

301 CGAGATTGTG TGCAAAATCA AATTTGCTGA GGAGGATGCA AAACCCAAGG

351 AGAAGGAGGC AGGGGATGAG CAGAGCCTCC TGGGGGCTGC TCAGGGGCCA

401 GCAGCCCCCTC GGGACCTGGC TACCTTTGCC AGCACCAGTA CTCTGCATGG

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451 GCTGGGCCGG GCCTGTGGCC CAGGCCCCCA TGGACTGCGC AGAACCTGT  
501 GGGTACTGGC CCTACTCACC TCACTGGCTG CCTTCCTGTA CCAGGCAGCC  
551 AGCCTGGCCA GGGGCTACCT GACCCGGCCT CACCTGGTAG CCATGGACCC  
601 TGCTGCCCCA GCCCCAGTGG CGGGCTTTCC GGCTGTCACC CTCTGCAACA  
651 TCAACCGCTT CCGGCATTCT GCACTCAGCG ATGCTGATAT CTTCCACCTG  
701 GCCAATCTGA CAGGGCTGCC CCCCAGAGAC CGGGATGGGC ACCGTGCAGC  
751 TGGCCTTCGC TACCCAGAGC CTGACATGGT AGACATCCTC AACCGCAGT  
801 GCCACCAGCT TGCTGACATG CTCAAGAGCT GCAACTTCAG TGGGCACCAC  
851 TGCTCCGCCA GCAACTTCTC TGTGGTCTAT ACTCGCTATG GAAAGTGTTA  
901 CACCTTCAAT GCAGATCCTC AGAGTTCACT GCCCAGCAGG GCAGGCGGCA  
951 TGGGTAGTGG CCTGGAGATC ATGCTAGACA TCCAGCAGGA GGAATACCTA  
1001 CCCATATGGA GGGAGACAAA TGAGACATCA TTCGAGGCAG GGATCCGGGT  
1051 GCAGATCCAC AGCCAGGAGG AGCCTCCCTA CATCCACCAG CTGGGGTTCTG  
1101 GTGTGTCCCC AGGCTTCCAG ACTTTTGTGT CCTGCCAGGA ACAGCGGCTA  
1151 ACTTATCTGC CCCAGCCTTG GGGCAACTGC CGGGCGGAAA GCAAGCTCAG  
1201 GGAGCCTGAG CTTCAGGGCT ACTCAGCCTA TAGTGTGTCT GCCTGCCGAC  
1251 TGCGCTGTGA GAAGGAGGCC GTGCTTCAGC GCTGCCACTG CCGGATGGTG  
1301 CACATGCCAG GCAATGAGAC CATCTGCCCG CCAAATATCT ACATTGAATG  
1351 TGCCGACCAC AACTGGACT CCCTGGGTGG GGGCTCTGAG GCGCCATGCT

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1401 TCTGCCCTAC ACCCTGCAAC CTGACTCGTT ACGGCAAAGA GATCTCCATG  
1451 GTCAAGATCC CCAACAGGGG CTCTGCCAGG TACCTGGCGA GGAAGTACAA  
1501 CCGCAATGAG ACCTACATAA GGGAAACTT CTTGGTCCTG GATGTCTTCT  
1551 TTGAGGCCCT AACCTCTGAA GCCATGGAAC AGCGAGCTGC CTATGGTCTG  
1601 TCAGCCTTGC TGGGGGACCT TGGGGGACAG ATGGGCCTGT TCATTGGGGC  
1651 TAGCATCCTC ACCTTGCTGG AGATCCTTGA CTACATCTAT GAGGTCTCCT  
1701 GGGATCGACT CAGAGGGTG TGGCGACGGC CCAAGACCCC ACTTAGGACG  
1751 TCCACTGGGG GCATCTCCAC TTTGGGGCTG CAGGAACTGA AGGAACAGAG  
1801 TCCCTGTCCA AATCGAGGCC GTGCTGAGGG TGGTGGGGCT AGCAACCTGC  
1851 TTCCCAACCA TCACCACCCC CACGGCCCCC CAGGAAGCCT CTTTGAAAAC  
1901 TTTGCTTGCT AGGATGGTGC TGTGTGGGGA AAGTACCCAT GAAACCCAC  
1951 ACTCTCCTAT TCCTGGGACA GAAGGTCTGG GGCAGCCCAG GGCTAAGGGA  
2001 AGGGGTGGTG CTCCTGAAA GGCCAGGACT AGGGTCCTGC TCTCCCTGAC  
2051 CTAGGCTCAG CTGCCTTGCA CAAGAATCCT TCTTGTCCAT ACTCCCTGCT  
2101 CCCAGGCAGG TGTCCAGGAA GGGCTAGAGA CCGGACTANG AGGCCCCTGA  
2151 GGAGGGGAGG GATGAAGAGA GGGAGGAAGG CGGAACCATG GTAGAGCCCC  
2201 TCNGTACATT TGTATATATT TAGGGACTGG GTGGGGGTGG GACACAGACA  
2251 TANAAGTTT GGGCTGCAGG GGAGGGTGAC ACAGGATAGT CAGGGTCCCA  
2301 ACCCTAATGG CANAANGCAA CTCCTTGGGA CCTAGGCATG TTGGGCTGGT

2351 TCTACTTCCC TCTTTCCAGG CCCAGCTCCC TCTTGGCATG GGGAGTGGGT  
2401 GGCCCATCAG GCCTGGCCCA GCTCCANTT CCCCCTGTAC CAGCCCCACC  
2451 ACAAGTTCCC TTCGTGGGGA GTGGGTGGAA ANACCTTTCA GACCTTGGCT  
2501 AAGCTTATGG GGAGANGGAG TGGCCTTCTC ANGCTTGCT CCCTANAGAC  
2551 TGGTTTTATA AANTGCTGGT GAACTTGGGA ATCNAGAGAC CCCNAGAAAA  
2601 AAAAAAAAAA AAAAAAAAAA AA

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 539 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SPASIC protein

1 MPIEIVCKIK FAEEDAKPKE KEAGDEQSLL GAAQGPAAPR DLATFASTST  
51 LHGLGRACGP GPHGLRRTLW VLALITSLAA FLYQAASLAR GYLTRPHLVA  
101 MDPAAPAPVA GPPAVTLCNI NRFRHSALSD ADIFHLANLT GLPPKDRDGH  
151 RAAGLRYPEP DMVDILNRTG HQLADMLKSC NFSGHHCSAS NFSVVYTRYG  
201 KCYTFNADPQ SSLPSRAGGM GSGLEIMLDI QQEYLPPIWR ETNETSFEAG  
251 IRVQIHSQEE PPYIHLGFG VSPGFQTFVS CQEQLTYLP QPWGNCRAES  
301 KLREPELQGY SAYSVSACRL RCEKEAVLQR CHCRMVHMPG NETICPPNIY

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351 IECADHTLDS LGGGSEGPCF CPTPCNLTRY GKEISMVKIP NRGSAARYLAR  
401 KYNRNETYIR ENFLVLDVFF EALTSEAMEQ RAAYGLSALL GDLGGQMGLF  
451 IGASILTLE ILDIYEVSW DRLKRVWRRP KTPLRTSTGG ISTLGLQELK  
501 EQSPCENRGR AEGGGASNLL PNHHHPHGPP GSLFENFAC

10 (2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 526 amino acids

(B) TYPE: Protein

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: ASIC protein

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SEQUENCE DESCRIPTION: SEQ ID NO: 3:

1 MELKTEEEV GGVQPVSQA FASSSTLHGL AHFSYERLS LKRALWALCF

51 LGSLAVLLCV CTERVQYYFC YHHVTKLDEV AASQLTFPAV TLCNLNEFRF

101 SQVSKNDLYH AGELLALLNN RYEIPDTQMA DEKQLEILQD KANFRSFKPK

151 PFNMREFYDR AGHDIRDMLL SCHFRGEACS AEDFKVVFTY YGKCYTFNSG

201 QDGRPRLKTM KGGTGNGLEI MLDIQQDEYL PVWGETDETS FEAGIKVQIH

251 SQDEPPFIDQ LGFGVAPGFQ TFVSCQEORL IYLPSPWGTC NAVTMDSDFF

301 DYSITACRI DCETRYLVEN CNCRMVHMPG DAPYCTPEQY KECADPALDF

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351 LVEKDQEYCV CEMPCNLTRY GKELSMVKIP SKASAKYLAK KFNKSEQYIG

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401 ENILVLDIFF EVLNYETIEQ KKAYEIAGLL GDIGGQMGLF IGASILTVLE  
451 LFDYAYEVIK HRLCRRGKCQ KEAKRSSADK GVALSLDDVK RHNPCESLRG  
501 HPAGMTYAAN ILPHHPARGT FEDFTC

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(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Rattus norvegicus

(F) TISSUE TYPE: Neurons

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TAGCAGTGAGGCTCTGGCCAGTCCCA

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(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Rattus norvegicus

(F) TISSUE TYPE: Dorsal root ganglion

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CCAGACCTTCTGTCCCAGGAATAGG

5 (2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

15 (vi) ORIGINAL SOURCE:

(A) ORGANISM: Rattus norvegicus

(F) TISSUE TYPE: Dorsal root ganglion

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

20 GACCTGGCTACCTTTGCCAGCACCA

(2) INFORMATION FOR SEQ ID NO: 7:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Rattus norvegicus

(F) TISSUE TYPE: neurons

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

8

ATATGGGTAGGTATTCTCTGCTG

## 2) INFORMATION FOR SEQ ID NO: 8:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Rattus norvegicus

(F) TISSUE TYPE: neurons

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

C/AGI,TAT/C,GG/CI,AAA/G,GAA/G,T/C/ATI,TCI,ATG

## 2) INFORMATION FOR SEQ ID NO: 9:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Rattus norvegicus

(F) TISSUE TYPE: neurons

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

IC/TT/A,IGC,ICC,IAT,A/GAA,IAG/A,ICC